

## In the Specification:

Replace the alignment starting on page 10, line 14 with the following alignment.

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gi|547724 INTERFERON ALPHA PRECURSOR (IFN-ALPHA) (SEQ ID NO:11)
gi|585317 INTERFERON DELTA-1 PRECURSOR (SEQ ID NO:12)
gi|124502 INTERFERON OMEGA-2 PRECURSOR (INTERFERON ALPHA-II-2) (SEQ ID NO:13)
gi|400061 INTERFERON OMEGA-1 PRECURSOR (INTERFERON ALPHA-II-1) (SEQ ID NO:14)

      10      20      30      40      50      60
NOV1a  L P K A Q V I S A L H K M H Q Q I F S L F L H K G L S D A W N R A F L D K L O T G F H Q Q L E D L E T C F G I E D C K
gi|547724 INTERFERON AS K A Q A T S V M H V T N Q K I P H F F C T E A S S A A W N T T L L E E F C T G L D R Q L T R L E A C V L Q E V E E
gi|585317 INTERFERON DE L Q E A Q A M S V L H E M L Q Q S F N L F H T E H S S A A W D T T L L E P C R T G L H Q Q L D N L E A C L G V M G E
gi|124502 INTERFERON OM F P E A Q A S V L H E M L Q Q I F S L F H T E R S S A A W N T T L L D E L C T G L R Q L E E L D T C L E Q E M G E
gi|400061 INTERFERON OM L Q K A H V M S V L H E M L Q Q I F S L F H T E R S S A A W N T T L L D Q L H T G L H Q Q L Q H L E T C L L V W G E
Consensus A Q S V L H M Q Q I F L F T E S S A A W N T L L T G L Q L L C Q G E

      70      80      90     100     110
NOV1a  Q E S A L E I E G P T L A K K R Y F Q G V H F E L K E R K E R N C T W E V V V M V K G E F L S T K L Q
gi|547724 INTERFERON AS G E A P L T N E D I H P E D S I L R N Y F Q R L S Y L Q E K K Y S P C A W E T V R A E I M R S L Y S S T A L Q
gi|585317 INTERFERON DE E E S A L G R T G P T L A K K R Y F Q G I H V Y L K E K Y S D C A W E T V R E I M R S F S S L I S L Q
gi|124502 INTERFERON OM E E S A L G T V R P T L A V K R Y F R G I H V Y L K E K K Y S D C A W E T V R M E I M R S F S S A N L Q
gi|400061 INTERFERON OM G E S A G A I S S P A L T L R Y F Q G I R V Y L K E K K Y S D C A W E V R M E I M K S L E L S T N M Q
Consensus SEQ ID NO:15 E S A L P L R Y F Q G Y L K E K K Y S C A W E V R E I M S L Q

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Replace the alignment starting on page 11, line 8 with the following alignment.

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gi|3318960|pdb|1AU1|A Chain A, Human Interferon-Beta Crystal Structure (SEQ ID NO:16)
gi|2624437|pdb|1RH2|A Chain A, Recombinant Human Interferon-Alpha 2b (SEQ ID NO:17)
gi|124432 INTERFERON ALPHA-1 PRECURSOR (SEQ ID NO:18)
gi|2147609 interferon-omega20 - rabbit (SEQ ID NO:19)
Consensus (SEQ ID NO:20)

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      10      20      30      40      50      60
NOV1a  D L P K A Q V I S A L H K M H Q Q I F S L F L H K G L S D A W N R A F L D K L O T G F H Q Q L E
gi|3318960|pdb| N E D I P E E I K Q L Q F O K E D A A L T T Y E M L Q N I F A L E R Q D S S S T G W N E T I V E N L L A N V Y H Q I N
gi|2624437|pdb| D F G F P Q E E F G N O F O K A E T T P V L H E M T Q Q I F N L F S T K D S S A A W D E T L L D K F Y T E L Y Q Q L N
gi|124432 INTER D F G F P Q E K V D A Q Q I K K A Q A I P V L S E L T Q Q I L N E T S K D S S A A W N A T L L D S F C N D L H Q Q L N
gi|2147609 inte D F G F P R E V V N G S Q F O K N O T V S V L H E M L Q Q I F N L L H T A R S S A A W N T T L L E E L H T A L H Q Q L Q
Consensus F P E Q K L E M Q Q I F F S S A W N T L Q Q L

      70      80      90     100     110
NOV1a  D L E T C F G I E D C K Q E S A L E I E G P T L A K K R Y F Q G V H F E L K E R K E R N C T W E V V
gi|3318960|pdb| H L K T V L E E K L E K E D F T R G K L M S S L H L K R Y M G R I L H Y L K A E M S H C A W T T V
gi|2624437|pdb| D L E A C V I Q G V G V T E T P L M N E D S L A V R K Y F Q R I T Y L K E K K Y S P C A W E V V
gi|124432 INTER D L Q G C L M Q Q V G V Q E F P L T Q E D A L A V R K Y F R I T Y L R E K K Y S P C A W E V V
gi|2147609 inte G L E T C L M Q A M G E E D S V L T A S P M L M L K R Y F Q R I R Y L D E K K Y S C A W E V V
Consensus L C G L L Y F R I Y L E K K S C A W E V

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Amend the paragraph starting on page 20, line 12 as follows.

**D3**  
This same alignment between KIAA1246 (SEQ ID NO:27) and NOV2 (identified as AF038458A) is shown below.

Replace the alignment starting on page 21, line 1 with the following alignment.

**D4**

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KIAA_predicted  --METLLGGLLAFQMA-----FAVVDACPKYCVCONLSESLGTLCPSKGLLFVPPDIIDRR
AF038458_A  MAIPLPLLCLLPLAPASSFPQSATPSPCFRRRCRCOTQSLPLSVLCFPGAGLLFVFPFSLDRR

KIAA_predicted  TVELRLGGNFIHISIQDFANMTGLVDLTLSRNTISHIQPFSFLDLLESLSLHLDNSRLP
RICK_AF038458_A AAEELRLADNFIASVRRERLANMTGLHLSLSRNTIRHYAAGAFADLRALRALHLDGNRLT

KIAA_predicted  SLGEDTLRGLVNLQHLIVNNNQLCGLADEAFEDFLLTLEDIDLSYNNLHGLPWDVSUREMV
AF038458_A  SLGEGQLRGLVNLRLHILSNNNQLAAAGALDDCAETLEDIDL-SYNNLEQLPWEALGELG

KIAA_predicted  NIHQLSLDHNLLDHIAEGTFADLQKLARLDLTSNRLQKLPEDPFFARSQASALTATPFAP
AF038458_A  NVENTGLDHNLLASVPAGAFSRLHKLARLDMTSNRETTLPEDPFLSELPLLARPRGSPAS

KIAA_predicted  PLSFSFGGNPLHCNCELLWLRRLERDDLETGSGFGGLKGRYFWHVREEEFVCEPFLITQ
AF038458_A  ALVLAFFGNPLHCNCELLWLRRLAERDDLEACASEPALGGRYFWAVGEEEFVCEPFPVTH

KIAA_predicted  HTHKLLWLEQAATLKCKANGDPSFLHWWAFDDRIVNNSRTAVYDNGTLDIFITTSQD
AF038458_A  RSPPLAW'AGRPAALRCRAVGDPERRVRWWSFQGRLLNNSSEARAEPNGTLELLVTEPGD

KIAA_predicted  SCAFTCIAANAAGEATAMVEVSIIVQLF--HLSNSTSRTAPPKSRLSDITGSSKTSRGGCG
AF038458_A  GGIFTCIAANAAGEATAAVELTVGPPFPFQLANSTSCDPP---RDGDPDALTPPSAASAS

KIAA_predicted  SGGGEPPESEPERAVLVSEVTTTSALWKWSVSKSAPRVKMYQLQYNCSDDDEVLYYRMIPA
AF038458_A  AKVADTG-PETDEGVQVTEHGATAALWQWPDQRPFGGRMYQLQYNSSADDLYYRMIPA

KIAA_predicted  SNKAFVNNLVSGTGVDLCVLAMWDDTATTLTATNIVGCAQFFTKADYPQCQSMHSQILG
AF038458_A  ESRSLELTDASGRTYDLCVLAVYEDSATGLTATRPVCCARESTEPALRPCGAPHAPFLG

KIAA_predicted  CTMILVIGGIVATLLVFIIVLLMVRYKWCNHEAF--SMAAAVSNWYSQTNGAQPPFPSS
AF038458_A  CTMIDALGGIVASVLVFIIVLLMVRYKWHGGQPPGKAKTPAPVSSVCSQTNGALGPTPT-

KIAA_predicted  APAGAPPQGPVKVVRNELLDFTASLARASDSSSSSSSLGSGEAAAGLGRAPWRIPPSAPRF
AF038458_A  ---PAPPAPFP-----AA-----LRAHTVVLQDCEPWGP GHEPVGP

KIAA_predicted  KPSLDRLMGAFASLDLKSQRKEELDSRTFAGRGAGTSARGHHSREPLLGPFAARARSL
AF038458_A  -----

KIAA_predicted  LPLPLEGKAKRSHSFDMGDFAAAAAGGVVPGGYSPPRKVSNIWTKRSLSVNGMLLPFEES
AF038458_A  -----

KIAA_predicted  DLVGARGTFGSSEWVMESTV
AF038458_A  -----
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Please replace the current sequence listing with the one enclosed.